

SEQUENCE LISTING

<110> Julius, David J.
Caterina, Michael J.
Brake, Anthony J.

<120> Nucleic acid sequences encoding
capsaicin receptor and capsaicin receptor-related
polypeptides and uses thereof

<130> UCAL084CON

<140> Unassigned

<141> 2001-10-15

<150> 09/235,451

<151> 1999-01-22

<150> 60/072,151

<151> 1998-01-22

<150> 08/915,461

<151> 1997-08-20

<160> 48

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2880

<212> DNA

<213> R. rattus

<400> 1

cagctccaag	gcacttgctc	catttgggg	gtgcctgcac	ctagctgggt	gcaaattggg	60
ccacagagga	tctggaaagg	atggaacaac	gggctagctt	agactcagag	gagtctgagt	120
ccccaccca	agagaactcc	tgcttgacc	ctccagacag	agaccctaac	tgcaagccac	180
ctccagtcaa	gccccacatc	ttcactacca	ggagtcgtac	ccggcttttt	gggaaggggtg	240
actcggagga	ggcctctccc	ctggactgcc	cttatgagga	aggcgggctg	gcttcctgcc	300
ctatcatcac	tgtcagctct	gttctaacta	tccagaggcc	tggggatgga	cctgccagtg	360
tcaggccgtc	atcccaggac	tccgtctccg	ctggtgagaa	gcccccgagg	ctctatgata	420
gcaggagcat	cttcgatgct	gtggctcaga	gtaactgcca	ggagctggag	agcctgctgc	480
ccttcctgca	gaggagcaag	aagcgctga	ctgacagcga	gttcaaagac	ccagagacag	540
gaaagacctg	tctgctaaaa	gccatgctca	atctgcacaa	tgggcagaat	gacaccatcg	600
ctctgctcct	ggacgttgcc	cgggaagacag	acagcctgaa	gcagtttgct	aatgccagct	660
acacagacag	ctactacaag	ggccagacag	cactgcacat	tgccattgaa	cggcggaaca	720
tgacgtgggt	gaccctcttg	gtggagaatg	gagcagatgt	ccaggctgcg	gctaacgggg	780
acttcttcaa	gaaaacccaa	gggaggcctg	gcttctactt	tggtagctg	cccctgtccc	840
tggctgcgtg	caccaaccag	ctggccattg	tgaagtccct	gctgcagaac	tcctggcagc	900
ctgcagacat	cagcgcccg	gactcagtgg	gcaacacggg	gcttcatgcc	ctgggtggagg	960

tggcagataa	cacagttgac	aacaccaagt	togtgacaag	catgtacaac	gagatcttga	1020
tcttgggggc	caaactccac	cccacgtga	agctggaaga	gatcaccaac	aggaaggggc	1080
tcacgccact	ggctctggct	gctagcagtg	ggaagatcgg	ggtcttggcc	tacattctcc	1140
agagggagat	ccatgaaccc	gagtgcgcgac	acctatccag	gaagttcacc	gaatgggcct	1200
atggggccagt	gcactcctcc	ctttatgacc	tgtcctgcat	tgacacctgt	gaaaagaact	1260
cggttctgga	ggtgatcgct	tacagcagca	gtgagacccc	taaccgtcat	gacatgcttc	1320
togtggaacc	cttgaaccga	ctcctacagg	acaagtggga	cagatttgct	aagcgcatct	1380
tctacttcaa	cttcttcgtc	tactgcttgt	atatgatcat	cttcaccgcg	gctgcctact	1440
atcggcctgt	ggaaggcttg	ccccctata	agctgaaaaa	caccgttggg	gactatttcc	1500
gagtcaaccg	agagatcttg	tctgtgtcag	gaggagtcta	cttcttcttc	cgaggggatc	1560
aataatttcc	gcagaggcga	ccatccctca	agagtttggt	tgtggacagc	tacagtgaga	1620
tacttttctt	tgtacagtcg	ctgttcacgc	tgggtgtctgt	ggtactgtac	ttcagccaac	1680
gcaaggagta	tgtggcttcc	atggtgttct	ccctggccat	gggctggacc	aacatgctct	1740
actatacccg	aggattccag	cagatgggca	tctatgctgt	catgattgag	aagatgatcc	1800
tcagagacct	gtgccgggtt	atgttcgtct	acctcggtgt	cttgtttggg	ttttccacag	1860
ctgtggtgac	actgattgag	gatgggaaga	ataactctct	gcctatggag	tccacaccac	1920
acaagtgcg	ggggtctgcc	tgcaagccag	gtaactctta	caacagcctg	tattccacat	1980
gtctggagct	gttcaagttc	accatcgga	tgggcgacct	ggagttcact	gagaactacg	2040
acttcaaggc	tgtcttcac	atcctgttac	tggcctatgt	gattctcacc	tacatccttc	2100
tgtctcaacat	gctcattgct	ctcatgggtg	agaccgtcaa	caagattgca	caagagagca	2160
agaacatctg	gaagctgcag	agagccatca	ccatccctga	tacagagaag	agcttctctga	2220
agtgcacag	gaaggccttc	cgctctggca	agctgctgca	ggtgggggtc	actcctgacg	2280
gcaaggatga	ctaccggtgg	tgtttcaggg	tggacgaggt	aaactggact	acctggaaca	2340
ccaatgtggg	tatcatcaac	gaggaccag	gcaactgtga	gggcgtcaag	cgcaccctga	2400
gcttctccct	gaggtcaggc	cgagtttcag	ggagaaaactg	gaagaacttt	gccctgggtc	2460
cccttctgag	ggatgcaagc	actcgagata	gacatgccac	ccagcaggaa	gaagttcaac	2520
tgaagcatta	tacgggatcc	cttaagccag	aggatgctga	ggttttcaag	gattccatgg	2580
tcccagggga	gaaataatgg	acactatgca	gggatcaatg	cggggtcttt	gggtgggtctg	2640
cttaggggaac	cagcaggggt	gacgttatct	gggtccactc	tgtgcctgcc	taggcacatt	2700
cctaggactt	cggcgggcct	gctgtgggaa	ctgggaggtg	tgtgggaatt	gagatgtgta	2760
tccaaccatg	atctccaaac	atttggtttt	caactcttta	tggactttat	taaacagagt	2820
gaatggcaaa	tctctacttg	gacacataaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	2880

<210> 2
 <211> 838
 <212> PRT
 <213> R. rattus

<400> 2

Met	Glu	Gln	Arg	Ala	Ser	Leu	Asp	Ser	Glu	Glu	Ser	Glu	Ser	Pro	Pro
1				5				10						15	
Gln	Glu	Asn	Ser	Cys	Leu	Asp	Pro	Pro	Asp	Arg	Asp	Pro	Asn	Cys	Lys
		20					25					30			
Pro	Pro	Pro	Val	Lys	Pro	His	Ile	Phe	Thr	Thr	Arg	Ser	Arg	Thr	Arg
		35				40					45				
Leu	Phe	Gly	Lys	Gly	Asp	Ser	Glu	Glu	Ala	Ser	Pro	Leu	Asp	Cys	Pro
	50				55					60					
Tyr	Glu	Glu	Gly	Gly	Leu	Ala	Ser	Cys	Pro	Ile	Ile	Thr	Val	Ser	Ser
65					70				75					80	
Val	Leu	Thr	Ile	Gln	Arg	Pro	Gly	Asp	Gly	Pro	Ala	Ser	Val	Arg	Pro

85															90					95				
Ser	Ser	Gln	Asp	Ser	Val	Ser	Ala	Gly	Glu	Lys	Pro	Pro	Arg	Leu	Tyr									
			100				105						110											
Asp	Arg	Arg	Ser	Ile	Phe	Asp	Ala	Val	Ala	Gln	Ser	Asn	Cys	Gln	Glu									
			115				120						125											
Leu	Glu	Ser	Leu	Leu	Pro	Phe	Leu	Gln	Arg	Ser	Lys	Lys	Arg	Leu	Thr									
			130				135						140											
Asp	Ser	Glu	Phe	Lys	Asp	Pro	Glu	Thr	Gly	Lys	Thr	Cys	Leu	Leu	Lys									
145				150						155			160											
Ala	Met	Leu	Asn	Leu	His	Asn	Gly	Gln	Asn	Asp	Thr	Ile	Ala	Leu	Leu									
			165						170			175												
Leu	Asp	Val	Ala	Arg	Lys	Thr	Asp	Ser	Leu	Lys	Gln	Phe	Val	Asn	Ala									
			180						185			190												
Ser	Tyr	Thr	Asp	Ser	Tyr	Tyr	Lys	Gly	Gln	Thr	Ala	Leu	His	Ile	Ala									
			195			200						205												
Ile	Glu	Arg	Arg	Asn	Met	Thr	Leu	Val	Thr	Leu	Leu	Val	Glu	Asn	Gly									
			210			215						220												
Ala	Asp	Val	Gln	Ala	Ala	Ala	Asn	Gly	Asp	Phe	Phe	Lys	Lys	Thr	Lys									
225				230						235			240											
Gly	Arg	Pro	Gly	Phe	Tyr	Phe	Gly	Glu	Leu	Pro	Leu	Ser	Leu	Ala	Ala									
			245						250			255												
Cys	Thr	Asn	Gln	Leu	Ala	Ile	Val	Lys	Phe	Leu	Leu	Gln	Asn	Ser	Trp									
			260			265						270												
Gln	Pro	Ala	Asp	Ile	Ser	Ala	Arg	Asp	Ser	Val	Gly	Asn	Thr	Val	Leu									
			275			280						285												
His	Ala	Leu	Val	Glu	Val	Ala	Asp	Asn	Thr	Val	Asp	Asn	Thr	Lys	Phe									
			290			295						300												
Val	Thr	Ser	Met	Tyr	Asn	Glu	Ile	Leu	Ile	Leu	Gly	Ala	Lys	Leu	His									
305				310						315			320											
Pro	Thr	Leu	Lys	Leu	Glu	Glu	Ile	Thr	Asn	Arg	Lys	Gly	Leu	Thr	Pro									
			325						330			335												
Leu	Ala	Leu	Ala	Ala	Ser	Ser	Gly	Lys	Ile	Gly	Val	Leu	Ala	Tyr	Ile									
			340			345						350												
Leu	Gln	Arg	Glu	Ile	His	Glu	Pro	Glu	Cys	Arg	His	Leu	Ser	Arg	Lys									
			355			360						365												
Phe	Thr	Glu	Trp	Ala	Tyr	Gly	Pro	Val	His	Ser	Ser	Leu	Tyr	Asp	Leu									
			370			375						380												
Ser	Cys	Ile	Asp	Thr	Cys	Glu	Lys	Asn	Ser	Val	Leu	Glu	Val	Ile	Ala									
385				390						395			400											
Tyr	Ser	Ser	Ser	Glu	Thr	Pro	Asn	Arg	His	Asp	Met	Leu	Leu	Val	Glu									
			405						410			415												
Pro	Leu	Asn	Arg	Leu	Leu	Gln	Asp	Lys	Trp	Asp	Arg	Phe	Val	Lys	Arg									
			420			425						430												
Ile	Phe	Tyr	Phe	Asn	Phe	Phe	Val	Tyr	Cys	Leu	Tyr	Met	Ile	Ile	Phe									
			435			440						445												
Thr	Ala	Ala	Ala	Tyr	Tyr	Arg	Pro	Val	Glu	Gly	Leu	Pro	Pro	Tyr	Lys									
			450			455						460												
Leu	Lys	Asn	Thr	Val	Gly	Asp	Tyr	Phe	Arg	Val	Thr	Gly	Glu	Ile	Leu									
465				470						475			480											
Ser	Val	Ser	Gly	Gly	Val	Tyr	Phe	Phe	Phe	Arg	Gly	Ile	Gln	Tyr	Phe									
			485						490			495												

Leu Gln Arg Arg Pro Ser Leu Lys Ser Leu Phe Val Asp Ser Tyr Ser
 500 505 510
 Glu Ile Leu Phe Phe Val Gln Ser Leu Phe Met Leu Val Ser Val Val
 515 520 525
 Leu Tyr Phe Ser Gln Arg Lys Glu Tyr Val Ala Ser Met Val Phe Ser
 530 535 540
 Leu Ala Met Gly Trp Thr Asn Met Leu Tyr Tyr Thr Arg Gly Phe Gln
 545 550 555 560
 Gln Met Gly Ile Tyr Ala Val Met Ile Glu Lys Met Ile Leu Arg Asp
 565 570 575
 Leu Cys Arg Phe Met Phe Val Tyr Leu Val Phe Leu Phe Gly Phe Ser
 580 585 590
 Thr Ala Val Val Thr Leu Ile Glu Asp Gly Lys Asn Asn Ser Leu Pro
 595 600 605
 Met Glu Ser Thr Pro His Lys Cys Arg Gly Ser Ala Cys Lys Pro Gly
 610 615 620
 Asn Ser Tyr Asn Ser Leu Tyr Ser Thr Cys Leu Glu Leu Phe Lys Phe
 625 630 635 640
 Thr Ile Gly Met Gly Asp Leu Glu Phe Thr Glu Asn Tyr Asp Phe Lys
 645 650 655
 Ala Val Phe Ile Ile Leu Leu Leu Ala Tyr Val Ile Leu Thr Tyr Ile
 660 665 670
 Leu Leu Leu Asn Met Leu Ile Ala Leu Met Gly Glu Thr Val Asn Lys
 675 680 685
 Ile Ala Gln Glu Ser Lys Asn Ile Trp Lys Leu Gln Arg Ala Ile Thr
 690 695 700
 Ile Leu Asp Thr Glu Lys Ser Phe Leu Lys Cys Met Arg Lys Ala Phe
 705 710 715 720
 Arg Ser Gly Lys Leu Leu Gln Val Gly Phe Thr Pro Asp Gly Lys Asp
 725 730 735
 Asp Tyr Arg Trp Cys Phe Arg Val Asp Glu Val Asn Trp Thr Thr Trp
 740 745 750
 Asn Thr Asn Val Gly Ile Ile Asn Glu Asp Pro Gly Asn Cys Glu Gly
 755 760 765
 Val Lys Arg Thr Leu Ser Phe Ser Leu Arg Ser Gly Arg Val Ser Gly
 770 775 780
 Arg Asn Trp Lys Asn Phe Ala Leu Val Pro Leu Leu Arg Asp Ala Ser
 785 790 795 800
 Thr Arg Asp Arg His Ala Thr Gln Gln Glu Glu Val Gln Leu Lys His
 805 810 815
 Tyr Thr Gly Ser Leu Lys Pro Glu Asp Ala Glu Val Phe Lys Asp Ser
 820 825 830
 Met Val Pro Gly Glu Lys
 835

<210> 3

<211> 2736

<212> DNA

<213> R. rattus

<400> 3

ggcgttaaac	ctgctctgtc	cactgtgtga	gacgaacagg	tggagggtgg	acgacgcaga	60
gaaagctcgg	agcgggcccgc	ggaggttccc	acagcccat	tactgtcagc	gttgagccgc	120
acccctccgg	gccgcacttc	ctctctcagt	ccccgctgcc	ggagagcccc	gctaggtctg	180
gtgatcctag	cctgcagttt	gccgcgcgta	caccttggt	tcagcctgcg	gggtcccagc	240
caggctgcc	cctgcggtat	gagagaggaa	ccttaacatc	tccatctcta	cagaggtttc	300
agctgtaagg	agcatcctcc	tctctcagga	tgacttcagc	ctccagcccc	ccagctttca	360
ggctggagac	ttccgatgga	gatgaagagg	gcaatgctga	ggtgaacaag	gggaagcagg	420
aaccgcccc	catggagtca	ccattccaga	gggaggaccg	gaattcctcc	cctcagatca	480
aagtgaacct	caacttcata	aagagacctc	ctaaaaacac	ttctgctccc	agccagcagg	540
agccagatcg	gtttgaccgt	gaccgactct	tcagtgtggt	ctcccggggt	gtccccgagg	600
aactgactgg	actgctagaa	tacctgcgct	ggaacagcaa	gtacctcact	gactctgcat	660
acacagaagg	ctccactgga	aagacgtgcc	tgatgaaggc	tgtgctgaac	cttcaggatg	720
gggtcaatgc	ctgcatcatg	ccgctgctgc	agattgacaa	ggattccggc	aatcccaagc	780
ccctcgtcaa	tgcccagtg	accgatgagt	tctaccaagg	ccacagtgcg	ctgcacatcg	840
ccatagagaa	gaggagcctg	cagtgcgtga	agctgctggt	agagaatgga	gcggtatgttc	900
acctccgagc	ctgtggccgc	ttcttccaaa	agcaccaagg	aacttgtttc	tattttggag	960
agctacctct	ttctctggct	gcggtcacca	agcagtggga	tgtggtgacc	tacctcctgg	1020
agaaccacac	ccagccggcc	agcctggagg	ccaccgactc	cctgggcaac	acagtctctgc	1080
atgctctggt	aatgattgca	gataactcgc	ctgagaacag	tgccctggtg	atccacatgt	1140
acgacgggt	tctacaaatg	ggggcgcgcc	tctgccccac	tgtgcagctt	gaggaaatct	1200
ccaaccacca	aggcctcaca	ccctgaaac	tagccgccaa	ggaaggcaaa	atcgagattt	1260
tcaggcacat	tctgcagcgg	gaattctcag	gaccgtacca	gcccctttcc	cgaaagttta	1320
ctgagtgggt	ttacggctct	gtgcgggtat	cgctgtacga	cctgtcctct	gtggacagct	1380
gggaaaagaa	ctcggtgctg	gagatcatcg	cttttcattg	caagagcccg	aaccggcacc	1440
gcatggtggt	tttagaacca	ctgaacaagc	ttctgcagga	gaaatgggat	cggctcgtct	1500
caagattctt	cttcaacttc	gcctgctact	tggtctacat	gttcattctc	accgtcgttg	1560
cctaccacca	gccttccctg	gatcagccag	ccatccctc	atcaaaagcg	acttttgggg	1620
aatccatgct	gctgctgggc	cacattctga	tctgtcttgg	gggtatttac	ctcttactgg	1680
gccagctgtg	gtacttttgg	cggcggcgcc	tgtttatctg	gatctcattc	atggacagct	1740
actttgaaat	cctcttttct	cttcaggctc	tgctcacagt	gctgtcccag	gtgctgcgct	1800
tcattggagac	tgaatggtac	ctaccctctg	tagtgttatc	cctagtgtctg	ggctggctga	1860
acctgcttta	ctacacacgg	ggcttttcagc	acacaggcat	ctacagtgtc	atgatccaga	1920
aggtcattct	tcgagacctg	ctccgtttcc	tgctggtcta	cctggtcttc	cttttcggct	1980
ttgctgtagc	cctagtaagc	ttgagcagag	aggcccgaag	tcccaaagcc	cctgaagata	2040
acaactccac	agtgcaggaa	cagcccacgg	tgggccagga	ggaggagcca	gctccatata	2100
ggagcattct	ggatgcctcc	ctagagctgt	tcaagttcac	cattggtatg	ggggagctgg	2160
ctttccagga	acagctgcgt	tttcgtgggg	tggtcctgct	gttgctgttg	gcctacgtcc	2220
ttctcaccta	cgctctgctg	ctcaacatgc	tcattgctct	catgagcgaa	actgtcaacc	2280
acgttgctga	caacagctgg	agcatctgga	agttgcagaa	agccatctct	gtcttggaag	2340
tggagaatgg	ttactggtgg	tgccggagga	agaaacatcg	tgaaggaggg	ctgctgaaag	2400
tcggcaccag	gggggatggt	acccctgatg	agcgtgggtg	cttcagggtg	gaggaagtaa	2460
attgggctgc	ttggggagaag	actcttccca	ccttatctga	ggatccatca	gggccaggca	2520
tcactggtaa	taaaaagaac	ccaacctcta	aaccggggaa	gaacagtgcc	tcagaggaag	2580
accatctgcc	ccttcagggtc	ctccagtccc	cctgatggcc	cagatgcagc	agcaggctgg	2640
caggatggag	tagggaatct	tcccagccac	accagaggct	actgaatttt	ggtggaaata	2700
taaatatattt	ttttgcataa	aaaaaaaaaa	aaaaaa			2736

5

COPIES

COPIES

Leu	Val	Tyr	Met	Phe	Ile	Phe	Thr	Val	Val	Ala	Tyr	His	Gln	Pro	Ser
				405					410					415	
Leu	Asp	Gln	Pro	Ala	Ile	Pro	Ser	Ser	Lys	Ala	Thr	Phe	Gly	Glu	Ser
			420					425					430		
Met	Leu	Leu	Leu	Gly	His	Ile	Leu	Ile	Leu	Leu	Gly	Gly	Ile	Tyr	Leu
		435					440					445			
Leu	Leu	Gly	Gln	Leu	Trp	Tyr	Phe	Trp	Arg	Arg	Arg	Leu	Phe	Ile	Trp
	450					455				460					
Ile	Ser	Phe	Met	Asp	Ser	Tyr	Phe	Glu	Ile	Leu	Phe	Leu	Leu	Gln	Ala
465					470					475				480	
Leu	Leu	Thr	Val	Leu	Ser	Gln	Val	Leu	Arg	Phe	Met	Glu	Thr	Glu	Trp
			485					490						495	
Tyr	Leu	Pro	Leu	Leu	Val	Leu	Ser	Leu	Val	Leu	Gly	Trp	Leu	Asn	Leu
		500						505					510		
Leu	Tyr	Tyr	Thr	Arg	Gly	Phe	Gln	His	Thr	Gly	Ile	Tyr	Ser	Val	Met
		515					520					525			
Ile	Gln	Lys	Val	Ile	Leu	Arg	Asp	Leu	Leu	Arg	Phe	Leu	Leu	Val	Tyr
	530					535					540				
Leu	Val	Phe	Leu	Phe	Gly	Phe	Ala	Val	Ala	Leu	Val	Ser	Leu	Ser	Arg
545					550					555					560
Glu	Ala	Arg	Ser	Pro	Lys	Ala	Pro	Glu	Asp	Asn	Asn	Ser	Thr	Val	Thr
				565					570					575	
Glu	Gln	Pro	Thr	Val	Gly	Gln	Glu	Glu	Glu	Pro	Ala	Pro	Tyr	Arg	Ser
			580					585					590		
Ile	Leu	Asp	Ala	Ser	Leu	Glu	Leu	Phe	Lys	Phe	Thr	Ile	Gly	Met	Gly
		595					600					605			
Glu	Leu	Ala	Phe	Gln	Glu	Gln	Leu	Arg	Phe	Arg	Gly	Val	Val	Leu	Leu
	610					615					620				
Leu	Leu	Leu	Ala	Tyr	Val	Leu	Leu	Thr	Tyr	Val	Leu	Leu	Leu	Asn	Met
625					630					635					640
Leu	Ile	Ala	Leu	Met	Ser	Glu	Thr	Val	Asn	His	Val	Ala	Asp	Asn	Ser
				645					650					655	
Trp	Ser	Ile	Trp	Lys	Leu	Gln	Lys	Ala	Ile	Ser	Val	Leu	Glu	Met	Glu
			660					665					670		
Asn	Gly	Tyr	Trp	Trp	Cys	Arg	Arg	Lys	Lys	His	Arg	Glu	Gly	Arg	Leu
		675					680					685			
Leu	Lys	Val	Gly	Thr	Arg	Gly	Asp	Gly	Thr	Pro	Asp	Glu	Arg	Trp	Cys
	690					695					700				
Phe	Arg	Val	Glu	Glu	Val	Asn	Trp	Ala	Ala	Trp	Glu	Lys	Thr	Leu	Pro
705					710					715					720
Thr	Leu	Ser	Glu	Asp	Pro	Ser	Gly	Pro	Gly	Ile	Thr	Gly	Asn	Lys	Lys
				725					730					735	
Asn	Pro	Thr	Ser	Lys	Pro	Gly	Lys	Asn	Ser	Ala	Ser	Glu	Glu	Asp	His
			740					745					750		
Leu															

<210> 5

<211> 273

<212> DNA

<213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(273)
 <223> n = A,T,C or G

<400> 5

tgcggtctcc	cnggggtgtc	cccgaggatc	tggctggact	tccnagagta	cctgagcaag	60
accagcaagt	acctcaccga	ctcgggaatac	acagagggct	ncnacaggta	agacgtgcct	120
gatgaaggct	gtgctgaacc	ttaaggacgg	ggtcaatgcc	tgcatctctgc	cactgctgca	180
gatcgachgg	gactctggca	atcctcagcc	cctggtaaata	gccagtgca	cagatgacta	240
ttaccgaggc	cacagcnctc	tgcacatcgc	cat			273

<210> 6
 <211> 768
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(768)
 <223> n = A,T,C or G

<400> 6

tcggtgagct	acccctctct	ttggccgctt	gcaccaagca	gtgggatgtg	gtaagctacc	60
tcttgagaa	cccacaccag	cccgccagcc	tgagnncac	tgactcccag	ggcaacacag	120
tctgcatgc	cctagtgatg	atctcggaca	actcagctga	gaacattgca	ctggtgacca	180
gcatgtatga	tgggtctctc	caagctgggg	cccgnccctc	gccctaccgt	gcnagcttga	240
ggacatccgc	aacctgcagg	atctcacgcc	tctgnaannt	ggccgccaag	gagggcaaga	300
tcgrrwtty	maggcacatc	ctnnsmagcg	ggrrktttca	ggactgnagc	cacctttnc	360
ccgaaagtto	accgagtgg	ngctannkcg	gcctgtccgg	gntgtcgctg	tnatgacctg	420
gnnyttctnt	ggacagctgt	naggagaact	cagtgtctgga	gatcattgcc	tttcattngc	480
aaragcccg	accgacaccg	aatggtcggt	ttggagcccc	tgaacaaact	gctgcaggcn	540
gaaatgggat	ctgctcatcc	ccaagttctt	cttaaaacttc	ctgtgtaatc	tgatntacat	600
gttcattctt	amckctgttg	cctaccatca	gcctaccnng	aagaagcagg	ccgccccctca	660
cctgaaagcg	gaggttgga	actccatgct	gctgacgggc	cacatcctta	tctgtctagg	720
ggggatctac	ctcctcgtgg	ggcaaaagtg	gaaattttgg	gggggaat		768

<210> 7
 <211> 650
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(650)
 <223> n = A,T,C or G

<400> 7

tgtttctctg	ccatcgagtg	gtacctgccc	ctgcttgtgt	ctgcgctgg	gctgggctgg	60
ctgaacctgc	tttactatac	acgtggcttc	cagcacacag	gcattctacag	tgatcatgatc	120
cagaagccct	ggtgagcctg	agccaggatt	ggcgccccga	agctcctaca	ggccccaatg	180


```

ccacagagtc agtgcagccc atggagggac aggaggacga gggcaacggg gccaggtaca 240
gggggtatcct ggwagcctcc ttggagctct tcaaattcac catcggcctg ggcgagctgg 300
ccttccaggc gcagctgcac ttccgcggca tnggtgctgc tgctgctnct ggcctacgtn 360
ctgctcacct acatcctgct gctcaacatg ctcatcgccc tcatngagcg agaccgtcaa 420
cankktcgcc actgacagct ggagcatctg gaagctgcag aaagncatct nntgtcctgg 480
agatggagaa tggctattgg tgggtcanga agaagcagcg ggcaggtgtg atgctganog 540
ttggcactaa gccagatggc agcccgatg agcgcctggtg cttcagggtn gaggaggtga 600
actgggcttc atngggagca gacgctgcct acgctgtgtg aggacccgct 650

```

```

<210> 8
<211> 317
<212> DNA
<213> Homo sapiens

```

```

<400> 8
gagcttctcc ctgcggtcaa gcagagtttc aggcagacac tggaagaact ttgccctggt 60
ccccctttta agagaggcaa gtctcgaata ggcagtctgc tcagcccgag gaagtttata 120
tgcgacagtt ttcaggtctc cttaaagccag aggacgctga ggtcttcaag agtctgccc 180
cttccgggga gaagtgagga cgtcacgcag acagcactgt caacactggg ccttaggaga 240
ccccgttgcc acgggggggt ctgaggggaa acagtgtctt ttcagcagcc ttgctggtct 300
ttgctgcccc gcatgtt 317

```

```

<210> 9
<211> 65
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> VARIANT
<222> (1)...(65)
<223> Xaa = Any Amino Acid

```

```

<400> 9
Ser Phe Ser Leu Arg Ser Ser Arg Val Ser Gly Arg His Trp Lys Asn
 1             5             10             15
Phe Ala Leu Val Pro Leu Leu Arg Glu Ala Ser Xaa Arg Xaa Arg Gln
          20          25          30
Ser Ala Gln Pro Glu Glu Val Tyr Leu Arg Gln Phe Ser Gly Ser Leu
          35          40          45
Lys Pro Glu Asp Ala Glu Val Phe Lys Ser Pro Ala Ala Ser Gly Glu
          50          55          60
Lys
65

```

```

<210> 10
<211> 471
<212> DNA
<213> M. musculus

```

```

<220>
<221> misc_feature

```

<222> (1)...(471)

<223> n = A,T,C or G

<400> 10

cctgcagaag	agcancangc	gcctgannga	cagcgagttc	aaagaccag	agacgggaaa	60
gacctgtctg	ctcaaagcca	tgctcaatct	gcacaatggg	cagaacgaca	ccattgctct	120
gctcctggac	attgcccgga	agacagatag	cctgaagcag	tttgtaaatg	ccagctacac	180
agacagctac	tacaagggcc	agacagcatt	acacattgcc	attgaaaggc	ggaacatggc	240
nctggtgacc	ctcttggtgg	agaatggagc	agatgtccag	gctgctgctg	acggggactt	300
cttcnanaaa	accaanggga	ggcctggcct	ctactttggg	gagctgcccc	tgtccctggc	360
tgcgtgcacc	aaccagctgg	ccattgtgaa	attcctgctg	cagaactcct	gggcagcctg	420
cagacatcag	tggcncggga	ttcngtgggc	aacacngtgc	tgacnccct	t	471

<210> 11

<211> 450

<212> DNA

<213> M. musculus

<400> 11

caagtgtcgg	ggatctgcct	tcgagggcca	agttaattct	ttacaacagc	ctgtattcca	60
catgtctgga	gctgttcaag	ttcaccatcg	gcatgggtga	cctggagttc	accgagaact	120
atgacttcaa	ggctgtcttt	catcatcctg	ttactggcct	atgtgattct	cacctacatc	180
ctcctgctca	acatgctcat	tgctctcatg	ggcgagactg	tcaacaagat	tcacaagag	240
agcaagaaca	tctggaagct	gcagcgagcc	atcaccatcc	tggatacaga	gaagagtttc	300
ctgaagtgca	tgaggaaggc	cttccgctcc	ggcaagctgc	tcaggtggg	gttcacgccg	360
gacggcaagg	atgacttccg	gtggtgcttc	aggggtggatg	aggtgaactg	gactacctgg	420
aacaccaacg	tgggcatcat	caacgaggac				450

<210> 12

<211> 18

<212> DNA

<213> R. rattus

<400> 12

gaccagcaag	tacctcac	18
------------	----------	----

<210> 13

<211> 49

<212> DNA

<213> R. rattus

<400> 13

ctcccatgca	gccagttta	cttccctcac	cctgaagcac	cagcgctca	49
------------	-----------	------------	------------	-----------	----

<210> 14

<211> 71

<212> PRT

<213> R. rattus

<400> 14

Glu Leu Phe Lys Phe Thr Ile Gly Met Gly Asp Leu Glu Phe Thr Glu

1 5 10 15
 Asn Tyr Asp Phe Lys Ala Val Phe Ile Ile Leu Leu Leu Ala Tyr Val
 20 25 30
 Ile Leu Thr Tyr Ile Leu Leu Leu Asn Met Leu Ile Ala Leu Met Gly
 35 40 45
 Glu Thr Val Asn Lys Ile Ala Gln Glu Ser Lys Asn Ile Trp Lys Leu
 50 55 60
 Gln Arg Ala Ile Thr Ile Leu
 65 70

<210> 15
 <211> 57
 <212> PRT
 <213> Homo sapiens

<400> 15
 Glu Leu Phe Lys Phe Thr Ile Gly Met Gly Glu Leu Ala Phe Gln Glu
 1 5 10 15
 Gln Leu His Phe Arg Gly Met Val Leu Leu Leu Leu Leu Ala Tyr Val
 20 25 30
 Leu Leu Thr Tyr Ile Leu Leu Leu Asn Met Leu Ile Ala Leu Met Ser
 35 40 45
 Glu Thr Val Asn Ser Val Ala Thr Asp
 50 55

<210> 16
 <211> 75
 <212> PRT
 <213> Caliphora

<400> 16
 Ser Leu Phe Trp Ala Ser Phe Gly Leu Val Asp Leu Val Ser Phe Asp
 1 5 10 15
 Leu Ala Gly Ile Lys Ser Phe Thr Arg Phe Trp Ala Leu Leu Met Phe
 20 25 30
 Gly Ser Tyr Ser Val Ile Asn Ile Ile Val Leu Leu Asn Met Leu Ile
 35 40 45
 Ala Met Met Ser Asn Ser Tyr Gln Ile Ile Ser Glu Arg Ala Asp Val
 50 55 60
 Glu Trp Lys Phe Ala Arg Ser Gln Leu Trp Met
 65 70 75

<210> 17
 <211> 75
 <212> PRT
 <213> D. melanogaster

<400> 17
 Ser Leu Phe Trp Ala Ser Phe Gly Leu Val Asp Leu Val Ser Phe Asp
 1 5 10 15
 Leu Ala Gly Ile Lys Ser Phe Thr Arg Phe Trp Ala Leu Leu Met Phe

		20						25					30				
Gly	Ser	Tyr	Ser	Val	Ile	Asn	Ile	Ile	Val	Leu	Leu	Asn	Met	Leu	Ile		
		35						40					45				
Ala	Met	Met	Ser	Asn	Ser	Tyr	Gln	Ile	Ile	Ser	Glu	Arg	Ala	Asp	Val		
		50				55					60						
Glu	Trp	Lys	Phe	Ala	Arg	Ser	Gln	Leu	Trp	Met							
65					70					75							

<210> 18
 <211> 75
 <212> PRT
 <213> B. taurus

Ser	Leu	Phe	Trp	Ser	Ile	Phe	Gly	Leu	Ile	Asn	Leu	Tyr	Val	Thr	Asn		
1				5				10					15				
Val	Lys	Ala	Gln	His	Glu	Phe	Thr	Glu	Phe	Val	Gly	Ala	Thr	Met	Phe		
			20					25					30				
Gly	Thr	Tyr	Asn	Val	Ile	Ser	Leu	Val	Val	Leu	Leu	Asn	Met	Leu	Ile		
		35					40					45					
Ala	Met	Met	Asn	Asn	Ser	Tyr	Gln	Leu	Ile	Ala	Asp	His	Ala	Asp	Ile		
		50				55					60						
Glu	Trp	Lys	Phe	Ala	Arg	Thr	Lys	Leu	Trp	Met							
65					70					75							

<210> 19
 <211> 61
 <212> PRT
 <213> C. elegans

Arg	Thr	Phe	Ile	Met	Thr	Ile	Gly	Glu	Phe	Ser	Val	Leu	Tyr	Arg	Glu		
1				5				10					15				
Met	Ser	Ala	Cys	Asp	Asn	Phe	Trp	Met	Lys	Trp	Ile	Gly	Lys	Leu	Ile		
			20					25					30				
Phe	Val	Ile	Phe	Glu	Thr	Phe	Val	Ser	Ile	Leu	Gln	Phe	Asn	Leu	Leu		
		35					40					45					
Ile	Ala	Met	Met	Thr	Arg	Thr	Tyr	Glu	Thr	Ile	Phe	Leu					
		50				55					60						

<210> 20
 <211> 350
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(350)
 <223> n = A,T,C or G

<400> 20

gagaggtcct	ggetggacnn	ngcagcctcc	tcctcctagg	atgacctcac	cctccagctc	60
tccagttttc	aggttggaga	cattagatgg	aggccaagaa	gatggctctg	aggcggacag	120
aggaaagctg	gattttggga	gcggtctgcc	tcccatggag	tcacagttcc	agggcgagga	180
ccggaaattc	gccccctcaga	taagagtcaa	cctcaactac	cgaaggggaa	caggtgccag	240
tcagccggat	ccaaaccgat	ttgaccgaga	tgggtctctc	aatgcgggtc	cccggggtgt	300
ccccgaggat	ctggctggac	ttccagagta	cctgagcaag	accagcaagt		350

<210> 21

<211> 764

<212> DNA

<213> Homo sapiens

<400> 21

tcggtgagct	acccctctct	ttggccgctt	gcaccaagca	gtgggatgtg	gtaagctacc	60
tcctggagaa	cccacaccag	cccgccagcc	tgcaggccac	tgactcccag	ggcaacacag	120
tcctgcatgc	cctagtgatg	atctcggaca	actcagctga	gaacattgca	ctggtgacca	180
gcatgtatga	tgggtctctc	caagctgggg	cccgcctctg	ccctaccgtg	cagcttgagg	240
acatccgcaa	cctgcaggat	ctcacgcctc	tgaagctggc	cgccaaggag	ggcaagatcg	300
rratyttcaa	ggcacatcct	tgcaagcggg	aagttttcag	gactgaagcc	accttttccc	360
cgaagattca	ccgagtgggtg	gctaattggg	cctgtccggg	ttgtcgctgt	aatgacctgg	420
gctttctgtg	gacagctgtg	aggagaactc	agtgtggrr	atcattgcct	ttcatttgca	480
aragcccagc	cgacaccgaa	tggctgtttt	ggagcccctg	aacaaactgc	tgcaggcgaa	540
atgggatctg	ctcatcccca	agttcttctt	aaacttctctg	tgtaatctga	ttacatgttc	600
atcttcaccg	ctgttgccca	ccatcagcct	accctgaaga	agcaggccgc	ccctcacctg	660
aaagcggagg	ttggaaactc	catgctgctg	acgggccaca	tccttatcct	gctagggggg	720
atctacctcc	tcgtggggca	aaagtggaaa	ttttgggggg	gaat		764

<210> 22

<211> 884

<212> DNA

<213> Homo sapiens

<400> 22

tgtttcctgg	ccatcgagtg	gtacctgccc	ctgcttgtgt	ctgcgctggt	gctgggctgg	60
ctgaacctgc	tttactatac	acgtggcttc	cagcacacag	gcatctacag	tgatcatgatc	120
cagaagccct	ggtgagcctg	agccaggatt	ggcgccccga	agctcctaca	ggccccaatg	180
ccacagagtc	agtgcagccc	atggagggac	aggaggacga	gggcaacggg	gcccagtaca	240
ggggatatcct	ggwagcctcc	ttggagctct	tcaaattcac	catcggcctg	ggcgagctgg	300
ccttccagga	gcagctgcac	ttccgcggca	tgggtctgct	gctgctgctg	gcctacgtgc	360
tgctcaccta	catcctgctg	ctcaacatgc	tcacgcctcc	cwtgagcgag	accgtcaaca	420
gtgtcgccac	tgacagctgg	agcatctgga	agctgcagaa	agccatctct	gtcctggaga	480
tggagaatgg	ctattgggtg	tgcaggaaga	agcagcgggc	aggtgtgatg	ctgaccgttg	540
gactaaagcc	agatggcagc	ccsgatgagc	gctgggtgctt	caggggtggag	gaggtgaact	600
gggcttcatg	ggagcagacg	ctgcctacgc	tgtgtgagga	cccgtcaggg	gcaggtgtcc	660
ctcgaaactct	cgagaaccct	gtcctggctt	cccctcccaa	ggaggatgag	gatggtgcct	720
ctgaggaaaa	ctatgtgccc	gtccagctcc	tccagtccaa	ctgatggccc	agatgcagca	780
ggaggccaga	ggacagagca	gaggatcttt	ccaaccacat	ctgctggctc	tggggtccca	840
gtgaattctg	gtggcaaata	tatatatttca	ctaammwmaa	aaac		884

<210> 23

<211> 727

<212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(727)
 <223> Xaa = Any Amino Acid

<400> 23
 Met Thr Ser Pro Ser Ser Ser Pro Val Phe Arg Leu Glu Thr Leu Asp
 1 5 10 15
 Gly Gly Gln Glu Asp Gly Ser Glu Ala Asp Arg Gly Lys Leu Asp Phe
 20 25 30
 Gly Ser Gly Leu Pro Pro Met Glu Ser Gln Phe Gln Gly Glu Asp Arg
 35 40 45
 Lys Phe Ala Pro Gln Ile Arg Val Asn Leu Asn Tyr Arg Lys Gly Thr
 50 55 60
 Gly Ala Ser Gln Pro Asp Pro Asn Arg Phe Asp Arg Asp Arg Leu Phe
 65 70 75 80
 Asn Ala Val Ser Arg Gly Val Pro Glu Asp Leu Ala Gly Leu Pro Glu
 85 90 95
 Tyr Leu Ser Lys Thr Ser Lys Tyr Leu Thr Asp Ser Glu Tyr Thr Glu
 100 105 110
 Gly Ser Thr Gly Lys Thr Cys Leu Met Lys Ala Val Leu Asn Leu Lys
 115 120 125
 Asp Gly Val Asn Ala Cys Ile Leu Pro Leu Leu Gln Ile Asp Arg Asp
 130 135 140
 Ser Gly Asn Pro Gln Pro Leu Val Asn Ala Gln Cys Thr Asp Asp Tyr
 145 150 155 160
 Tyr Arg Gly His Ser Ala Leu His Ile Ala Ile Glu Lys Arg Ser Leu
 165 170 175
 Gln Cys Val Lys Leu Leu Val Glu Asn Gly Ala Asn Val His Ala Arg
 180 185 190
 Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 195 200 205
 Gly Glu Leu Pro Leu Ser Leu Ala Ala Cys Thr Lys Gln Trp Asp Val
 210 215 220
 Val Ser Tyr Leu Leu Glu Asn Pro His Gln Pro Ala Ser Leu Gln Ala
 225 230 235 240
 Thr Asp Ser Gln Gly Asn Thr Val Leu His Ala Leu Val Met Ile Ser
 245 250 255
 Asp Asn Ser Ala Glu Asn Ile Ala Leu Val Thr Ser Met Tyr Asp Gly
 260 265 270
 Leu Leu Gln Ala Gly Ala Arg Leu Cys Pro Thr Val Gln Leu Glu Asp
 275 280 285
 Ile Arg Asn Leu Gln Asp Leu Thr Pro Leu Lys Leu Ala Ala Lys Glu
 290 295 300
 Gly Lys Ile Xaa Ile Phe Xaa Arg His Ile Leu Ala Ser Gly Lys Phe
 305 310 315 320
 Ser Gly Leu Lys Pro Pro Phe Pro Arg Lys Phe Thr Glu Trp Trp Leu
 325 330 335

Met	Gly	Pro	Val	Arg	Val	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa		
			340					345					350				
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa		
		355					360					365					
Pro	Asp	Arg	His	Arg	Met	Val	Val	Leu	Glu	Pro	Leu	Asn	Lys	Leu	Leu		
	370					375					380						
Gln	Ala	Lys	Trp	Asp	Leu	Leu	Ile	Pro	Lys	Phe	Phe	Leu	Asn	Phe	Leu		
385					390					395					400		
Cys	Asn	Leu	Xaa	Tyr	Met	Phe	Ile	Phe	Thr	Ala	Val	Ala	Tyr	His	Gln		
				405					410					415			
Pro	Thr	Leu	Lys	Lys	Gln	Ala	Ala	Pro	His	Leu	Lys	Ala	Glu	Val	Gly		
		420						425					430				
Asn	Ser	Met	Leu	Leu	Thr	Gly	His	Ile	Leu	Ile	Leu	Leu	Gly	Gly	Ile		
	435						440						445				
Tyr	Leu	Leu	Val	Gly	Gln	Lys	Trp	Lys	Phe	Trp	Xaa	Xaa	Xaa	Xaa	Xaa		
	450					455					460						
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Pro	Gly	His	Arg	Val	
465					470						475					480	
Val	Pro	Ala	Pro	Ala	Cys	Val	Cys	Ala	Gly	Ala	Gly	Leu	Ala	Glu	Pro		
				485					490					495			
Ala	Leu	Leu	Tyr	Thr	Trp	Leu	Pro	Ala	His	Arg	His	Leu	Gln	Cys	His		
			500					505					510				
Asp	Pro	Glu	Ala	Leu	Val	Ser	Leu	Ser	Gln	Asp	Trp	Arg	Pro	Glu	Ala		
	515						520					525					
Pro	Thr	Gly	Pro	Asn	Ala	Thr	Glu	Ser	Val	Gln	Pro	Met	Glu	Gly	Gln		
	530					535						540					
Glu	Asp	Glu	Gly	Asn	Gly	Ala	Gln	Tyr	Arg	Gly	Ile	Leu	Xaa	Ala	Ser		
545				550						555					560		
Leu	Glu	Leu	Phe	Lys	Phe	Thr	Ile	Gly	Met	Gly	Glu	Leu	Ala	Phe	Gln		
				565					570					575			
Glu	Gln	Leu	His	Phe	Arg	Gly	Met	Val	Leu	Leu	Leu	Leu	Leu	Ala	Tyr		
			580				585						590				
Val	Leu	Leu	Thr	Tyr	Ile	Leu	Leu	Leu	Asn	Met	Leu	Ile	Ala	Leu	Xaa		
	595					600						605					
Ser	Glu	Thr	Val	Asn	Ser	Val	Ala	Thr	Asp	Ser	Trp	Ser	Ile	Trp	Lys		
	610					615					620						
Leu	Gln	Lys	Ala	Ile	Ser	Val	Leu	Glu	Met	Glu	Asn	Gly	Tyr	Trp	Trp		
625				630						635					640		
Cys	Arg	Lys	Lys	Gln	Arg	Ala	Gly	Val	Met	Leu	Thr	Val	Gly	Thr	Lys		
				645					650					655			
Pro	Asp	Gly	Ser	Pro	Asp	Glu	Arg	Trp	Cys	Phe	Arg	Val	Glu	Glu	Val		
		660				665						670					
Asn	Trp	Ala	Ser	Trp	Glu	Gln	Thr	Leu	Pro	Thr	Leu	Cys	Glu	Asp	Pro		
	675					680						685					
Ser	Gly	Ala	Gly	Val	Pro	Arg	Thr	Leu	Glu	Asn	Pro	Val	Leu	Ala	Ser		
	690					695				700							
Pro	Pro	Lys	Glu	Asp	Glu	Asp	Gly	Ala	Ser	Glu	Glu	Asn	Tyr	Val	Pro		
705				710						715					720		
Val	Gln	Leu	Leu	Gln	Ser	Asn											
				725													

<210> 24
 <211> 2845
 <212> DNA
 <213> chicken

<400> 24
 ttccatata acagagggag tttgctgaga ctggactatt ctgcagaaga caggatattt 60
 ttgcaatatt tgggtgatcgg acggagggac acagaaaact tgaaaggctg cttgttcatc 120
 atgtcttcca ttcttgagaa gatgaagaaa tttggcagtt ctgacataga agaactctgaa 180
 gtgacagatg aacacacgga tggggaagac tcagcactgg aaacagctga caacctccag 240
 ggtacattca gcaacaaggt gcagccatcc aaaagcaaca tctttgcaag acgtggacgg 300
 tttgtgatgg gggattgtga caaggacatg gctccaatgg actcctttta ccagatggat 360
 cacctgatgg caccttctgt catcaaattt catgccata tggagagggg gaaacttcac 420
 aagctcctgt caacagactc catcacaggg tgctctgaaa aagctttcaa attttatgac 480
 cgcagaagga tctttgatgc tgtagcccgga ggcagcacaaggacctgga tgatctgctg 540
 ctctatctaa ataggacctt gaagcatctc acagatgatg aattcaaaga accagaaaact 600
 gggaaaacct gcttactgaa agccatgctg aatctacatg atgggaaaaa tgataccatt 660
 cccttgctgc tggatattgc aaagaaaact ggaactctga aagagtttgt aaatgcagaa 720
 tatactgaca actattacaa aggccagact gcactccaca ttgccattga gagaaggaaac 780
 atgtacctgg taaaactctt ggtccagaat ggagcagatg ttcatgcaag agcatgtggg 840
 gagttcttca ggaaaatcaa agggaaaacct ggtttttatt ttggagagct gcccctgtcc 900
 ctggctgcct gcaccaatca gctctgcatt gtgaaatttc tccttgagaa cccctaccag 960
 gctgctgaca ttgctgctga ggactccatg ggcaatatgg ttctgcatac tctgggtggag 1020
 attgcagata atactaagga taataccaag ttcgttacga agatgtacaa taacatattg 1080
 atccttggtg ccaaaaataaa tcctatcctg aagttggaag aactcaccaa caaaaaaggg 1140
 ctgactccat taacgttggc agccaaaaca ggggaagatag ggattttcgc ttacatcctc 1200
 agacgagaga tcaaagatcc tgaatgcaga cacttgtcta ggaagtccac tgaatgggct 1260
 tatggacctg tccattcatc tctttatgac ctgtcctgca tagacacatg tgagaaaaat 1320
 tcagtgettg aaattattgc ctacagtagt gaaacaccaa atcgtcatga gatgctgctg 1380
 gtagagcccc ttaacaggct actgcaagac aagtgggacc gatttgtcaa gcacttattt 1440
 tacttcaact tctttgtata tgcaattcat atcagcatcc tcaccacagc tgcctactac 1500
 agacctgtgc agaaggggga caagcctccc ttcgcttttg gtcacagcac tgggggaatat 1560
 tttcgagtga ctggagagat actgagtgtg ttgggaggac tgtatttttt tttcagaggg 1620
 atacagtatt ttgtgcagag gcgcccatac ttgaagacgc tgatagttga cagttacagt 1680
 gaagttcttt tcttcgttca ctctttgctc ctctgagct ctgtgggtgct gtacttctgt 1740
 ggccaggaac tgtatgtggc ttccatgggtc ttctccttgg ctctgggctg ggctaacatg 1800
 ctatactaca cccgtggctt ccagcagatg ggcatttact ctgtcatgat tgcaaagatg 1860
 atcctaagag acttatgtcg cttcatgttt gtctatctag tattcctctt gggattttcc 1920
 acagctgtgg tgactttaat tgaagatgac aatgaggggc aggacacaaa tagctctgaa 1980
 tatgcccgat gcagccatac gaaacgaggc cgcacatcct ataacagtct gtattatacc 2040
 tgcttggaac ttttcaagtt cactattggg atgggagacc tggagtttac agagaactac 2100
 aggttcaagt ctgtgtttgt catccttttg gttctctatg tcatccttac gtacatcctc 2160
 ctgctcaata tgcttattgc actgatggga gaaactgtga gcaaaattgc acaggagagc 2220
 aagagcatct ggaaactcca gagggccatc acgatcttgg atattgaaaa cagctacttg 2280
 aactgtttga ggcgctcatt ccgatctgga aaaagagtct tgggtgggaat cacacctgat 2340
 ggccaagatg attacagatg gtgctttaga gttgatgaag tgaactggtc cacgtggaat 2400
 acaaatttgg gcataatcaa cgaagatcct ggggtgctctg gtgacctcaa acgaaatccc 2460
 agttactgta ttaagcctgg tagagtttca gggaaaaatt ggaaaacttt ggttccactt 2520
 ttaagagatg gaagcaggag agaagaaaca ccaaaactac cagaagaaat caaattaaaa 2580
 cccatttttg aaccttatta tgagccagag gattgtgaga cattgaagga atcgcttcca 2640
 aagtcagtct gatcttttgt ttttaagaag gtttaattcta gttgtttgtg ttggttctta 2700

caaggaggac aattaaaacg cttccttcat aagagcgggg atttatggaa aaaggccaaa 2760
gaagctagga aatgactgtg tgcaaggatt cattaagtat cttgaataaa ctacttggtg 2820
tttaaaaaaa aaaaaaaaaa aaaaa 2845

<210> 25
<211> 843
<212> PRT
<213> chicken

<400> 25
Met Ser Ser Ile Leu Glu Lys Met Lys Lys Phe Gly Ser Ser Asp Ile
1 5 10 15
Glu Glu Ser Glu Val Thr Asp Glu His Thr Asp Gly Glu Asp Ser Ala
20 25 30
Leu Glu Thr Ala Asp Asn Leu Gln Gly Thr Phe Ser Asn Lys Val Gln
35 40 45
Pro Ser Lys Ser Asn Ile Phe Ala Arg Arg Gly Arg Phe Val Met Gly
50 55 60
Asp Cys Asp Lys Asp Met Ala Pro Met Asp Ser Phe Tyr Gln Met Asp
65 70 75 80
His Leu Met Ala Pro Ser Val Ile Lys Phe His Ala Asn Met Glu Arg
85 90 95
Gly Lys Leu His Lys Leu Leu Ser Thr Asp Ser Ile Thr Gly Cys Ser
100 105 110
Glu Lys Ala Phe Lys Phe Tyr Asp Arg Arg Arg Ile Phe Asp Ala Val
115 120 125
Ala Arg Gly Ser Thr Lys Asp Leu Asp Asp Leu Leu Leu Tyr Leu Asn
130 135 140
Arg Thr Leu Lys His Leu Thr Asp Asp Glu Phe Lys Glu Pro Glu Thr
145 150 155 160
Gly Lys Thr Cys Leu Leu Lys Ala Met Leu Asn Leu His Asp Gly Lys
165 170 175
Asn Asp Thr Ile Pro Leu Leu Leu Asp Ile Ala Lys Lys Thr Gly Thr
180 185 190
Leu Lys Glu Phe Val Asn Ala Glu Tyr Thr Asp Asn Tyr Tyr Lys Gly
195 200 205
Gln Thr Ala Leu His Ile Ala Ile Glu Arg Arg Asn Met Tyr Leu Val
210 215 220
Lys Leu Leu Val Gln Asn Gly Ala Asp Val His Ala Arg Ala Cys Gly
225 230 235 240
Glu Phe Phe Arg Lys Ile Lys Gly Lys Pro Gly Phe Tyr Phe Gly Glu
245 250 255
Leu Pro Leu Ser Leu Ala Ala Cys Thr Asn Gln Leu Cys Ile Val Lys
260 265 270
Phe Leu Leu Glu Asn Pro Tyr Gln Ala Ala Asp Ile Ala Ala Glu Asp
275 280 285
Ser Met Gly Asn Met Val Leu His Thr Leu Val Glu Ile Ala Asp Asn
290 295 300
Thr Lys Asp Asn Thr Lys Phe Val Thr Lys Met Tyr Asn Asn Ile Leu
305 310 315 320
Ile Leu Gly Ala Lys Ile Asn Pro Ile Leu Lys Leu Glu Glu Leu Thr

Asn	Lys	Lys	Gly	Leu	Thr	Pro	Leu	Thr	Leu	Ala	Ala	Lys	Thr	Gly	Lys
			340					345					350		
Ile	Gly	Ile	Phe	Ala	Tyr	Ile	Leu	Arg	Arg	Glu	Ile	Lys	Asp	Pro	Glu
		355					360					365			
Cys	Arg	His	Leu	Ser	Arg	Lys	Phe	Thr	Glu	Trp	Ala	Tyr	Gly	Pro	Val
	370					375					380				
His	Ser	Ser	Leu	Tyr	Asp	Leu	Ser	Cys	Ile	Asp	Thr	Cys	Glu	Lys	Asn
385					390					395					400
Ser	Val	Leu	Glu	Ile	Ile	Ala	Tyr	Ser	Ser	Glu	Thr	Pro	Asn	Arg	His
			405						410					415	
Glu	Met	Leu	Leu	Val	Glu	Pro	Leu	Asn	Arg	Leu	Leu	Gln	Asp	Lys	Trp
			420					425					430		
Asp	Arg	Phe	Val	Lys	His	Leu	Phe	Tyr	Phe	Asn	Phe	Phe	Val	Tyr	Ala
		435					440					445			
Ile	His	Ile	Ser	Ile	Leu	Thr	Thr	Ala	Ala	Tyr	Tyr	Arg	Pro	Val	Gln
	450					455					460				
Lys	Gly	Asp	Lys	Pro	Pro	Phe	Ala	Phe	Gly	His	Ser	Thr	Gly	Glu	Tyr
465					470				475						480
Phe	Arg	Val	Thr	Gly	Glu	Ile	Leu	Ser	Val	Leu	Gly	Gly	Leu	Tyr	Phe
			485						490					495	
Phe	Phe	Arg	Gly	Ile	Gln	Tyr	Phe	Val	Gln	Arg	Arg	Pro	Ser	Leu	Lys
			500					505					510		
Thr	Leu	Ile	Val	Asp	Ser	Tyr	Ser	Glu	Val	Leu	Phe	Phe	Val	His	Ser
		515					520					525			
Leu	Leu	Leu	Leu	Ser	Ser	Val	Val	Leu	Tyr	Phe	Cys	Gly	Gln	Glu	Leu
	530					535					540				
Tyr	Val	Ala	Ser	Met	Val	Phe	Ser	Leu	Ala	Leu	Gly	Trp	Ala	Asn	Met
545					550				555						560
Leu	Tyr	Tyr	Thr	Arg	Gly	Phe	Gln	Gln	Met	Gly	Ile	Tyr	Ser	Val	Met
			565						570					575	
Ile	Ala	Lys	Met	Ile	Leu	Arg	Asp	Leu	Cys	Arg	Phe	Met	Phe	Val	Tyr
			580					585					590		
Leu	Val	Phe	Leu	Leu	Gly	Phe	Ser	Thr	Ala	Val	Val	Thr	Leu	Ile	Glu
		595					600					605			
Asp	Asp	Asn	Glu	Gly	Gln	Asp	Thr	Asn	Ser	Ser	Glu	Tyr	Ala	Arg	Cys
	610					615					620				
Ser	His	Thr	Lys	Arg	Gly	Arg	Thr	Ser	Tyr	Asn	Ser	Leu	Tyr	Tyr	Thr
625					630					635					640
Cys	Leu	Glu	Leu	Phe	Lys	Phe	Thr	Ile	Gly	Met	Gly	Asp	Leu	Glu	Phe
			645						650					655	
Thr	Glu	Asn	Tyr	Arg	Phe	Lys	Ser	Val	Phe	Val	Ile	Leu	Leu	Val	Leu
			660					665					670		
Tyr	Val	Ile	Leu	Thr	Tyr	Ile	Leu	Leu	Leu	Asn	Met	Leu	Ile	Ala	Leu
		675					680								

Ile	Thr	Pro	Asp	Gly	Gln	Asp	Asp	Tyr	Arg	Trp	Cys	Phe	Arg	Val	Asp
			740					745					750		
Glu	Val	Asn	Trp	Ser	Thr	Trp	Asn	Thr	Asn	Leu	Gly	Ile	Ile	Asn	Glu
		755					760					765			
Asp	Pro	Gly	Cys	Ser	Gly	Asp	Leu	Lys	Arg	Asn	Pro	Ser	Tyr	Cys	Ile
	770					775					780				
Lys	Pro	Gly	Arg	Val	Ser	Gly	Lys	Asn	Trp	Lys	Thr	Leu	Val	Pro	Leu
785					790					795					800
Leu	Arg	Asp	Gly	Ser	Arg	Arg	Glu	Glu	Thr	Pro	Lys	Leu	Pro	Glu	Glu
				805					810					815	
Ile	Lys	Leu	Lys	Pro	Ile	Leu	Glu	Pro	Tyr	Tyr	Glu	Pro	Glu	Asp	Cys
			820					825					830		
Glu	Thr	Leu	Lys	Glu	Ser	Leu	Pro	Lys	Ser	Val					
		835					840								

<210> 26
 <211> 135
 <212> DNA
 <213> Homo sapiens

<400> 26	
ttcaagtttta cgatcgggat gggcgacctg gagttcactg agaactatga cttcaaggct	60
gtcttcatca tctgtctgct ggcctatgta attctcacct acatcctcct gctcaacatg	120
tttatogetc tcatg	135

<210> 27
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> consensus

<400> 27	
tttcaaagtt tcacgatcat atcgggatca tg	32

<210> 28
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> consensus

<400> 28	
catgatcaga gatcgcgata tgatcagaca tagtt	35

<210> 29
 <211> 135
 <212> DNA
 <213> chicken

<400> 29
 ttcaagttca cgattgggat gggtgacctg gattttcatg aacatgccag attcagatac 60
 tttgtcatgc ttctgctgct gctttttgtg atcctcacct acatcctttt gctcaacatg 120
 cttatagccc ttata 135

<210> 30
 <211> 135
 <212> DNA
 <213> chicken

<400> 30
 ttcaagttca ctattgggat gggagacctg gagtttacag agaactacag gttcaagtct 60
 gtgtttgtca tccttttggg tctctatgct atccttacgt acatcctcct gctcaatatg 120
 cttatagccc taatg 135

<210> 31
 <211> 28
 <212> DNA
 <213> Homo sapiens

<400> 31
 tatctttcaa tctttctttc gtgatcta 28

<210> 32
 <211> 17
 <212> DNA
 <213> Homo sapiens

<400> 32
 aaaaggggga ccaggggc 17

<210> 33
 <211> 2544
 <212> DNA
 <213> Homo sapiens

<400> 33
 ggatccagca aggatgaaga aatggagcag cacagacttg ggggcagctg cggaccact 60
 ccaaaaggac acctgcccag acccctgga tggagaccct aactccaggc cacctccagc 120
 caagccccag ctctccacgg ccaagagccg caccggctc tttgggaagg gtgactcga 180
 ggaggctttc ccggtggatt gccctcacga ggaaggtag ctggactcct gcccgaccat 240
 cacagtcagc cctgttatca ccatccagag gccaggagac ggccccaccg gtgccaggct 300
 gctgtcccag gactctgtcg ccgccagcac cgagaagacc ctcaggctct atgatcgag 360
 gagtatcttt gaagccgttg ctcagaataa ctgccaggat ctggagagcc tgctgtctt 420
 cctgcagaag agcaagaagc acctcacaga caacgagttc aaagaccctg agacagggaa 480
 gacctgtctg ctgaaagcca tgctcaacct gcacgacgga cagaacacca ccatccccct 540
 gctcctggag atcgcgcggc aaaogagacag cctgaaggag cttgtcaacg ccagctacac 600
 ggacagctac tacaagggcc agacagcact gcacatcgcc atcgagagac gcaacatggc 660
 cctggtgacc ctctggtgg agaacggagc agacgtccag gctgcggccc atggggactt 720
 ctttaagaaa accaaagggc ggcttgatt ctacttcggg gaactgcccc tgtccttggc 780
 cgcgtgcacc aaccagctgg gcatcgtgaa gttcctgctg cagaactcct ggcagacggc 840


```

gaccgagatc ggctcttcaa tgcggtctcc cgggggtgtcc ccgaggatct ggctggactt 300
ccagagtacc tgagcaagac cagcaagtac ctcaccgact cggaatacac agaggggtcc 360
acaggtaaga cgtgcctgat gaaggctgtg ctgaacctta aggacggagt caatgcctgc 420
attctgccac tgctgcagat cgacagggac tctggcaatc ctcagcccct ggtaaatagcc 480
cagtgcacag atgactatta ccgaggccac agcgctctgc acatcgccat tgagaagagg 540
agtctgcagt gtgtgaagct cctggtggag aatggggcca atgtgcatgc ccggggcctgc 600
ggcgcgttct tccagaaggg ccaagggact tgcttttatt tcggtgagct acccctctct 660
ttggcgcgtt gcaccaagca gtgggatgtg gtaagctacc tcctggagaa cccacaccag 720
cccgcagcc tgcaggccac tgactcccag ggcaacacag tcctgcatgc cctagtgatg 780
atctoggaca actcagctga gaacattgca ctggtgacca gcatgtatga tgggctcctc 840
caagctgggg cccgcctctg ccctaccgtg cagcttgagg acatccgcaa cctgcaggat 900
ctcacgcctc tgaagctggc cgccaaggag ggcaagatcg agattttcag gcacatcctg 960
cagcgggagt tttcaggact gagccacctt tcccgaagt tcaccgagtg gtgctatggg 1020
cctgtccggg tgctcgtgta tgacctggct tctgtggaca gctgtgagga gaactcagtg 1080
ctggagatca ttgcctttca ttgcaagagc ccgcaccgac accgaatggg cgttttggag 1140
cccctgaaca aactgctgca ggcgaaatgg gatctgctca tcccgaagt cttcttaaac 1200
ttcctgtgta atctgatcta catgttcata ttcaccgctg ttgcctacca tcagcctacc 1260
ctgaagaagc aggcgcgcc tccactgaaa gcggaggttg gaaactccat gctgctgacg 1320
ggccacatcc ttatcctgct agggggggatc tacctcctcg tgggccagct gtggtacttc 1380
tggcggcgcc acgtgttcat ctggatctcg ttcatagaca gctactttga aatcctcttc 1440
ctgttccagg ccctgctcac agtggtgtcc caggtgctgt gtttcttggc catcgagtgg 1500
tacctgcccc tgcttgtgtc tgcgctgggtg ctgggctggc tgaacctgct ttactataca 1560
cgtggtctcc agcacacagg catctacagt gtcatgatcc agaaggcat cctgcgggac 1620
ctgctgcgct tccttctgat ctacttagtc ttccttttcg gcttcgctgt agccctgggtg 1680
agcctgagcc aggaggtctg gcgccccgaa gctcctacag gcccgaatgc cacagagtca 1740
gtgcagccca tggagggaca ggaggacgag ggcaacgggg ccagtagacg gggatatcctg 1800
gaagcctcct tggagctctt caaattcacc atcggcattg gcgagctggc cttccaggag 1860
cagctgcact tccgcggcat ggtgctgctg ctgctgctgg cctacgtgct gctcacctac 1920
atcctgctgc tcaacatgct catcgccctc atgagcgaga ccgtcaacag tgctgccact 1980
gacagctgga gcatctggaa gctgcagaaa gccatctctg tcctggagat ggagaatggc 2040
tattggtggt gcaggaagaa gcagcgggca ggtgtgatgc tgaccgttg gactaagcca 2100
gatggcagcc ccgatgagcg ctggtgcttc aggggtggagg aggtgaactg ggcttcatgg 2160
gagcagacgc tgcctacgct gtgtgaggac ccgtcagggg caggtgtccc tcgaactctc 2220
gagaaccttg tcctggcttc ccctcccaag gaggatgagg atggtgcctc tgaggaaaac 2280
tatgtgcccg tccagctcct ccagtcacaac tgatggccca gatgcagcag gaggccagag 2340
gacagagcag aggatctttc caaccacatc tgctggctct 2380

```

<210> 36
 <211> 764
 <212> PRT
 <213> Homo sapiens

```

<400> 36
Met Thr Ser Pro Ser Ser Pro Val Phe Arg Leu Glu Thr Leu Asp
 1           5           10           15
Gly Gly Gln Glu Asp Gly Ser Glu Ala Asp Arg Gly Lys Leu Asp Phe
      20           25           30
Gly Ser Gly Leu Pro Pro Met Glu Ser Gln Phe Gln Gly Glu Asp Arg
      35           40           45
Lys Phe Ala Pro Gln Ile Arg Val Asn Leu Asn Tyr Arg Lys Gly Thr
      50           55           60

```


465		470		475		480									
Thr	Val	Val	Ser	Gln	Val	Leu	Cys	Phe	Leu	Ala	Ile	Glu	Trp	Tyr	Leu
		485		490		495									
Pro	Leu	Leu	Val	Ser	Ala	Leu	Val	Leu	Gly	Trp	Leu	Asn	Leu	Leu	Tyr
		500		505		510									
Tyr	Thr	Arg	Gly	Phe	Gln	His	Thr	Gly	Ile	Tyr	Ser	Val	Met	Ile	Gln
		515		520		525									
Lys	Val	Ile	Leu	Arg	Asp	Leu	Leu	Arg	Phe	Leu	Leu	Ile	Tyr	Leu	Val
		530		535		540									
Phe	Leu	Phe	Gly	Phe	Ala	Val	Ala	Leu	Val	Ser	Leu	Ser	Gln	Glu	Ala
		545		550		555									
Trp	Arg	Pro	Glu	Ala	Pro	Thr	Gly	Pro	Asn	Ala	Thr	Glu	Ser	Val	Gln
		565		570		575									
Pro	Met	Glu	Gly	Gln	Glu	Asp	Glu	Gly	Asn	Gly	Ala	Gln	Tyr	Arg	Gly
		580		585		590									
Ile	Leu	Glu	Ala	Ser	Leu	Glu	Leu	Phe	Lys	Phe	Thr	Ile	Gly	Met	Gly
		595		600		605									
Glu	Leu	Ala	Phe	Gln	Glu	Gln	Leu	His	Phe	Arg	Gly	Met	Val	Leu	Leu
		610		615		620									
Leu	Leu	Leu	Ala	Tyr	Val	Leu	Leu	Thr	Tyr	Ile	Leu	Leu	Leu	Asn	Met
		625		630		635									
Leu	Ile	Ala	Leu	Met	Ser	Glu	Thr	Val	Asn	Ser	Val	Ala	Thr	Asp	Ser
		645		650		655									
Trp	Ser	Ile	Trp	Lys	Leu	Gln	Lys	Ala	Ile	Ser	Val	Leu	Glu	Met	Glu
		660		665		670									
Asn	Gly	Tyr	Trp	Trp	Cys	Arg	Lys	Lys	Gln	Arg	Ala	Gly	Val	Met	Leu
		675		680		685									
Thr	Val	Gly	Thr	Lys	Pro	Asp	Gly	Ser	Pro	Asp	Glu	Arg	Trp	Cys	Phe
		690		695		700									
Arg	Val	Glu	Glu	Val	Asn	Trp	Ala	Ser	Trp	Glu	Gln	Thr	Leu	Pro	Thr
		705		710		715									
Leu	Cys	Glu	Asp	Pro	Ser	Gly	Ala	Gly	Val	Pro	Arg	Thr	Leu	Glu	Asn
		725		730		735									
Pro	Val	Leu	Ala	Ser	Pro	Pro	Lys	Glu	Asp	Glu	Asp	Gly	Ala	Ser	Glu
		740		745		750									
Glu	Asn	Tyr	Val	Pro	Val	Gln	Leu	Leu	Gln	Ser	Asn				
		755		760											

<210> 37
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 37
 ggcgcacctgg agttcactga g

21

<210> 38
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 38
gagcaggagg atgtaggtga g 21

<210> 39
<211> 226
<212> DNA
<213> Homo sapiens

<400> 39
ctgcagcttc cagatgttct tgctctcctg tgcgatcttg ttgacagtct caccatgag 60
ggcgatgagc atgttgagca ggaggatgta ggtgagaatt acataggcca gcagcaggat 120
gatgaagaca gccttgaagt catagtcttc agtgaactcc aggtcgcca tgccgatggt 180
gaacttgaac agctccaggc aggtggagta caggctgttg taggag 226

<210> 40
<211> 226
<212> DNA
<213> R. rattus

<400> 40
gagaatgttg tcggacataa ggtgtacaga cctcgacaag ttcaagtggg agccgtaccc 60
gctggacctc aagtgactct tgatgctgaa gttccgacag aagtagtagg acaatgaccg 120
gatacactaa gagtggatgt aggaagacga gttgtacgag taacgagagt acccactctg 180
gcagttgttc taacgtgttc tctcgttctt gtagaccttc gacgtc 226

<210> 41
<211> 145
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(145)
<223> n = A,T,C or G

<400> 41
aagacctcag cgtcctctgg cttcagagac cctgnaaaac tgcgcagat aaacttcttc 60
gggctgagca nactgcctat ctcgagcact tgcctctctt aaaaggggga ccagggcaaa 120
gttcttccag tgtctgacct aaact 145

<210> 42
<211> 144
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(144)
<223> n = A,T,C or G

<400> 42

tcaaagtcg tctgtgacct tcttgaaacg ggaccagggg gaaaattctc tccgttcang 60
 agctntatcc gtcagacgag tcgggctcct tcaaatagac gctgtcaaaa gtcccagaga 120
 tttcggtctc ctgcgactcc agaa 144

<210> 43
 <211> 219
 <212> DNA
 <213> Homo sapiens

<400> 43
 cccactccaa aaggacacct gccagacccc cctggatgga gaccctaact ccaggccacc 60
 tccagccaag cccagctct ccacggccaa gagccgcacc cggctctttg ggaaggggtga 120
 ctggaggag gctttcccg tggattgccc tcacgaggaa ggtgagctgg actcctgccc 180
 gaccatcaca gtcagccctg ttatcaccat ccagaggcc 219

<210> 44
 <211> 219
 <212> DNA
 <213> R. rattus

<400> 44
 cccaccccaa gagaactcct gcctggaccc tccagacaga gaccctaact gcaagccacc 60
 tccagtcaag cccacatct tcaactaccag gagtcgtacc cggctttttg ggaaggggtga 120
 ctggaggag gcctctcccc tggactgccc ttatgaggaa ggcgggctgg cttcctgccc 180
 tatcatcact gtcagctctg ttctaactat ccagaggcc 219

<210> 45
 <211> 91
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(91)
 <223> Xaa = Any Amino Acid

<400> 45
 Met Lys Lys Trp Ser Ser Thr Asp Leu Gly Ala Ala Ala Asp Pro Leu
 1 5 10 15
 Gln Lys Asp Thr Cys Pro Asp Pro Leu Asp Gly Asp Pro Asn Ser Arg
 20 25 30
 Pro Pro Pro Ala Lys Pro Gln Leu Ser Thr Ala Lys Ser Arg Thr Arg
 35 40 45
 Leu Phe Gly Lys Gly Asp Ser Glu Glu Ala Phe Pro Val Asp Cys Pro
 50 55 60
 His Glu Glu Gly Glu Leu Asp Ser Cys Pro Thr Ile Thr Val Ser Pro
 65 70 75 80
 Val Ile Thr Ile Gln Arg Pro Arg Xaa Arg Pro
 85 90

<210> 46

<211> 91
 <212> PRT
 <213> R. rattus

<400> 46
 Met Glu Gln Arg Ala Ser Leu Asp Ser Glu Glu Ser Glu Ser Pro Pro
 1 5 10 15
 Gln Glu Asn Ser Cys Leu Asp Pro Pro Asp Arg Asp Pro Asn Cys Lys
 20 25 30
 Pro Pro Pro Val Lys Pro His Ile Phe Thr Thr Arg Ser Arg Thr Arg
 35 40 45
 Leu Phe Gly Lys Gly Asp Ser Glu Glu Ala Ser Pro Leu Asp Cys Pro
 50 55 60
 Tyr Glu Glu Gly Gly Leu Ala Ser Cys Pro Ile Ile Thr Val Ser Ser
 65 70 75 80
 Val Leu Thr Ile Gln Arg Pro Gly Asp Gly Pro
 85 90

<210> 47
 <211> 24
 <212> DNA
 <213> Homo sapiens

<400> 47
 agaaatggag cagcacagac ttgg

24

<210> 48
 <211> 23
 <212> DNA
 <213> Homo sapiens

<400> 48
 tcactttctcc ccggaagcgg cag

23